

FIGURE 1

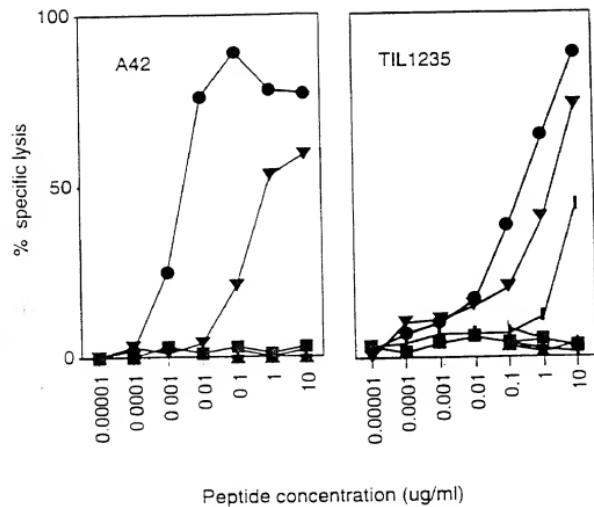


FIGURE 2

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FIGURE 3A

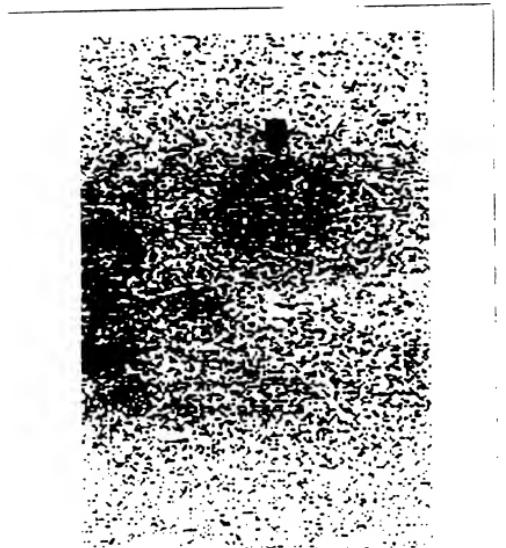
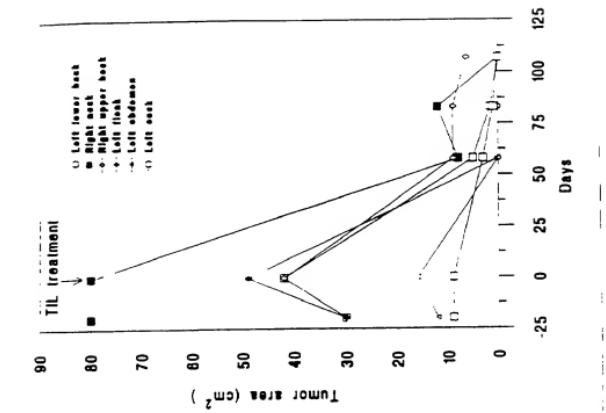


FIGURE 3B



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GTCGACGGCC	ATTACCAATC	GCGACCGGGG	AGAACACAAT	40
<u>GGATCTGGTG</u>	CTAAAAAGAT	GCCTTCTTCA	TTGGCTGTG	80
ATAGGTGCTT	TGCTGGCTGT	GGGGGCTACA	AAAGTACCCA	120
GAAACCAGGA	CTGGCTGGT	GCTCAAGGC	AACTCAGAAC	160
CAAAGCCTGG	AACAGGCAGC	TGTATCCAGA	GTGGACAGAA	200
GCCCCAGAGAC	TTGACTGCTG	GAGAGGTGGT	CAAGTGTCCC	240
TCAAGGTCAG	TAATGATGGG	CCTACACTGA	TTGGTGCAAA	280
TGCCTCCTTC	TCTATTGCCT	TGAACCTCCC	TGGAAGCCAA	320
AAGGTATTGC	CAGATGGGCA	GGTTATCTGG	GTCAACAAATA	360
CCATCATCAA	TGGGAGGCCAG	GTGTGGGGAG	GACAGCCAGT	400
GTATCCCCAG	GAAACTGACG	ATGCCTGCAT	CTTCCCTGAT	440
GGTGGACCTT	GCCCCATCTGG	CTCTTGGTCT	CAGAAGAGAA	480
GCTTTGTTA	TGTCTGGAAG	ACCTGGGGCC	AATACTGGCA	520
ATTTCTAGGG	GGCCCACTGT	CTGGGCTGAG	CATTGGGACA	560
GGCAGGGCAA	TGCTGGGCAC	ACACACCATG	GAAGTGTACTG	600
TCTACCACATCG	CCGGGGATCC	CGGAGCTATG	TGCCTCTTGC	640
TCATTCCAGC	TCAGCCTTCA	CCATTACTGA	CCAGGTGCCT	680
TTCTCCGTGA	GGCGTGTCCC	GTTCGGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACCT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCCTC	TCACCCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAACATGCAG	AGGCCCCCTAA	1000
CACCAACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGGGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120

FIGURE 4

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TGCACCTGTG	CAGATGCCAA	CTGCAGAGAG	CACAGGTATG	116
ACACCTGAGA	AGGTGCCAGT	TTCAGAGGTC	ATGGGTACCA	120
CACTGGCAGA	GATGTCAACT	CCAGAGGCTA	CAGGTATGAC	124
ACCTGCAGAG	GTATCAATTG	TGGTGCTTTC	TGGAACCACA	128
GCTGCACAGG	TAACAACATAC	AGAGTGGGTG	GAGACCACAG	132
CTAGAGAGCT	ACCTATCCCT	GAGCCTGAAG	GTCCAGATGC	136
CAGCTCAATC	ATGTCTACGG	AAAGTATTAC	AGGTTCCCTG	140
GGCCCCCTGC	TGGATGGTAC	AGCCACCTTA	AGGCTGGTGA	144
AGAGACAAGT	CCCCCTGGAT	TGTGTTCTGT	ATCGATATGG	148
TTCCCTTTCC	GTCACCCCTGG	ACATTGTCCA	GGGTATTGAA	152
AGTGCCGAGA	TCCTGCAGGC	TGTGCCGTCC	GGTGAGGGGG	156
ATGCATTTGA	GCTGACTGTG	TCCTGCCAAG	GCGGGCTGCC	160
CAAGGAAGCC	TGCATGGAGA	TCTCATGCC	AGGGTGCCAG	164
CCCCCTGCC	AGCGGCTGTG	CCAGCCTGTG	CTACCCAGCC	168
CAGCCTGCCA	GCTGGTTCTG	CACCAAGATAC	TGAAGGGTGG	172
CTCGGGGACA	TACTGCCCTCA	ATGTGTCTCT	GGCTGATACC	176
AACAGCCTGG	CAGTGGTCAG	CACCCAGCTT	ATCATGCC	180
GTCAAGAACG	AGGCCTTGGG	CAGGTTCCGC	TGATCGTGGG	184
CATCTTGCTG	GTGTTGATGG	CTGTGGTCT	TGCATCTCTG	188
ATATATAGGC	GCAGACTTAT	GAAGCAAGAC	TTCTCCGTAC	192
CCCAGTGCC	ACATAGCAGC	AGTCACTGGC	TGCGTCTACC	196
CCGCATCTTC	TGCTCTTGTC	CCATTGGTGA	GAACAGCCCC	200
CTCCTCAGTG	GGCAGCAGGT	CTGAGTACTC	TCATAT <u>GATG</u>	204
CTGTGATTTT	CCTGGAGTTG	ACAGAAACAC	CTATATTTCC	208
CCCAGTCTTC	CCTGGGAGAC	TACTATTAAC	TGAAATAAAT	212
ACTCAGAGCC	TGAAAAAAA	TAAAAAAA	AAAAAAA	216
AAAAAAAAAA	AA			2172

FIGURE 4 (continued)

FIGURE 5A

1 MDLVLKRCIL HLAVIGALLA VGATKVRNQ DWLGVSROLR TKA
51 EWTTEAQRDLC WRGGQVSLKV SNDGFTLIGA NASFSIALNF PGSKVLPDG
101 QVIWVNNTII NGSQVWGGOP VYFQETTDAC IFPDGCPCS GSWSOKRSFV
151 YWVKIWGQYI QFLGGPVSGL SIGTGRAMLG THIMEVTYH RRGRSRYVPL
201 AHSSSAFTIT DQVPPFSVSVS QILRALDGGNK HFLRNQPLTF ALQLHDPGSY
251 LAEADLSYTW DFGDSSGTII SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVPGTT DGHRTAEEP NTTAGQVPTT EVVGTTPGQA PTAEPSTGTT
351 VQVPVTEVIS TAPVQMPTEA STGMTPERVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIIVL SGTTAAQVTT TEWVETTARE LPIPEPEGD ASSIMSTESI
451 TGSLGPLLDG TATTELRVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDGF ELTVSCQGGL PKEACMEIIS PGCCOPAQL CQPVLPSPAC
551 QLVHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGVPLIV
601 GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCP
651 ENSPLLSGQQ V

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FIGURE 5B

Pmell7 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----.....
gp100 M-----V-----Q-----L-----.....
cDNA25FL M-----F-----Q-----L-----.....
cDNA25TR M-----F-----Q-----L-----.....
1 162 236 274 588 649
Q-----L-----.....-PPQWAAGLSTLI

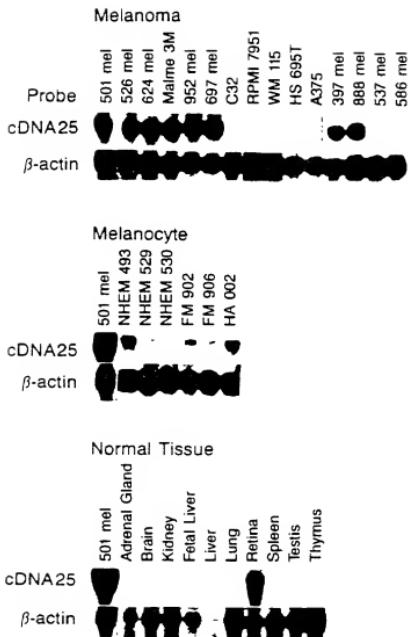


FIGURE 6